



1633
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TECH CENTER 1600/2900

CERTIFICATE OF MAILING

I HEREBY CERTIFY THAT THIS CORRESPONDENCE IS BEING DEPOSITED
WITH THE UNITED STATES POSTAL SERVICE AS FIRST-CLASS MAIL IN AN
ENVELOPE ADDRESSED TO: ASSISTANT COMMISSIONER FOR PATENTS
WASHINGTON, D.C. 20231, ON APRIL 17, 2001

Karen Moon Bruce
AGENT/ATTORNEY FOR APPLICANT

April 17, 2001
DATE

Docket No. 1134C

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

Applicant: Duvick, et al. Date: April 17, 2001
Serial No.: 09/771,045 Group Art Unit: 1633
Filed January 26, 2001 Examiner:
For: "Amino Polyol Amine Oxidase Polynucleotides and Related Polypeptides and
Methods of Use"

Assistant Commissioner for Patents
Washington, D.C. 20231

TRANSMITTAL

Transmitted herewith are the following documents: Response to Notice to Comply;
Substitute computer readable form (CFR) copy of the Sequence Listing; Substitute paper copy of
Sequence Listing; and Statement to Support Filing and Submission in Accordance with 37 CFR
§§ 1.821 through 1.825.

Although there should be no fees associated with the filing of these documents the
Commissioner is hereby authorized to charge any processing fees associated with said
documents, or to credit any overpayment, to Deposit Account 16-1852. A duplicate copy of this
sheet is enclosed.

Respectfully submitted,

Karen Moon Bruce

Karen Moon Bruce
Agent for Applicant(s)
Registration No. 42,366

PIONEER HI-BRED INTERNATIONAL, INC.
Corporate Intellectual Property
7100 N.W. 62nd Avenue
P.O. Box 1000
Johnston, Iowa 50131-1000
Phone: (515) 248-4879
Facsimile: (515) 334-6883



CERTIFICATE OF MAILING

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Kan M. B.
AGENT/ATTORNEY FOR APPLICANT

April 17, 2001
DATE

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Docket No. 1134C

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

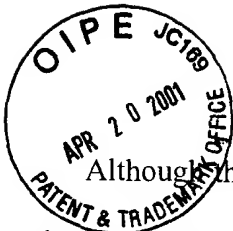
Applicant: Duvick, et al. Date: April 17, 2001
Serial No.: 09/771,045 Group Art Unit: 1633
Filed January 26, 2001 Examiner:
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Assistant Commissioner for Patents
Washington, D.C. 20231

RESPONSE TO NOTICE TO COMPLY WITH REQUIREMENTS
FOR PATENT APPLICATIONS CONTAINING NUCLEOTIDE SEQUENCE
AND/OR AMINO ACID SEQUENCE DISCLOSURES

This letter is in response to the "Notice to Comply" mailed on March 29, 2001 which indicated that the copy of the "Sequence Listing" in computer readable form does not comply with the requirements of 37 C.F.R. 1.822 and/or 1.823. A copy of "The Notice to Comply" is enclosed.

Enclosed please find a substitute computer readable form (CFR) copy of the "Sequence Listing", a substitute paper copy of the "Sequence Listing", and a statement that the content of the paper and computer readable copies are the same, and where applicable, include no new matter.



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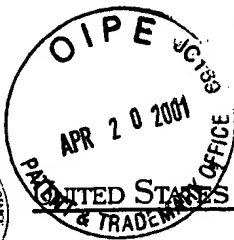
Although there should be no fees associated with this Response the Commissioner is hereby authorized to charge any processing fees associated with said Response, or to credit any overpayment, to Deposit Account 16-1852.

Respectfully submitted,

Karen Moon Bruce
Agent for Applicant(s)
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APR 24 2001

 COMMISSIONER FOR PATENTS
 UNITED STATES PATENT AND TRADEMARK OFFICE
 TECH CENTER 1600/2800
 WASHINGTON, D.C. 20231
 www.uspto.gov

APPLICATION NUMBER	FILING/RECEIPT DATE	FIRST NAMED APPLICANT	ATTORNEY DOCKET NUMBER
09/771,045	01/26/2001	Jonathan P. Duvick	1134C

CONFIRMATION NO. 7253

FORMALITIES LETTER



OC000000005917489

Pioneer Hi-Bred International, Inc.
 Corporate Intellectual Property
 7100 N.W. 62nd Avenue
 P.O. Box 1000
 Johnston, IA 50131-1000

Date Mailed: 03/29/2001

NOTICE TO COMPLY WITH REQUIREMENTS FOR PATENT APPLICATIONS CONTAINING NUCLEOTIDE SEQUENCE AND/OR AMINO ACID SEQUENCE DISCLOSURES

Applicant is given TWO MONTHS FROM THE DATE OF THIS NOTICE within which to file the items indicated below to avoid abandonment. Extensions of time may be obtained under the provisions of 37 CFR 1.136(a).

- A copy of the "Sequence Listing" in computer readable form has been submitted. However, the content of the computer readable form does not comply with the requirements of 37 C.F.R. 1.822 and/or 1.823, as indicated on the attached copy of the marked -up "Raw Sequence Listing." Applicant must provide a substitute computer readable form (CRF) copy of the "Sequence Listing" and a statement that the content of the sequence listing information recorded in computer readable form is identical to the written (on paper or compact disc) sequence listing and, where applicable, includes no new matter, as required by 37 CFR 1.821(e), 1.821(f), 1.821(g), 1.825(b), or 1.825(d).

For questions regarding compliance to these requirements, please contact:

- For Rules Interpretation, call (703) 308-4216
- To Purchase PatentIn Software, call (703) 306-2600
- For PatentIn Software Program Help, call (703) 306-4119 or e-mail at patin21help@uspto.gov or patin3help@uspto.gov

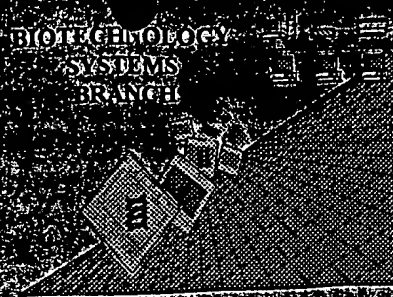
*A copy of this notice **MUST** be returned with the reply.*

Customer Service Center

Initial Patent Examination Division (703) 308-1202

PART 1 - ATTORNEY/APPLICANT COPY

RAW SEQUENCE LISTING ERROR REPORT



The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer-readable form:

Application Serial Number: 09/97,045
Source: OIP
Date Processed by STIC: 2/8/2001

BEST AVAILABLE COPY

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRI SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENT IN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)

PATENT IN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

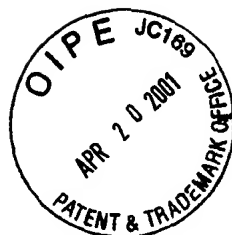
TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE **CHECKER VERSION 3.0 PROGRAM**, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW.

Checker Version 3.0

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR 1.821-1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS based version of Checker and is Y2K compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker to review the sequence listing is expected to result in fewer errors in sequence listings thus saving time and money.

Checker Version 3.0 can be downloaded from the USPTO website at the following address:
<http://www.uspto.gov/web/offices/pat/checker>



OIPE

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/771,045

DATE: 02/08/2001
TIME: 12:14:08

Input Set : A:\1134CSEQLIST.TXT
Output Set: N:\CRF3\02082001\I771045.raw

Does Not Comply
Corrected Diskette Needed.

P-6

4 <110> APPLICANT: Duvick, Jonathan P.
5 Gilliam, Jacob T.
6 Maddox, Joyce R.
8 <120> TITLE OF INVENTION: Amino Polyol Amine Oxidase
9 Polynucleotides and Related Polypeptides and Methods of Use
12 <130> FILE REFERENCE: 1134C
C--> 14 <140> CURRENT APPLICATION NUMBER: US/09/771,045
C--> 14 <141> CURRENT FILING DATE: 2001-01-26
14 <150> PRIOR APPLICATION NUMBER: US 60/092,936
15 <151> PRIOR FILING DATE: 1998-07-15
17 <150> PRIOR APPLICATION NUMBER: US 60/135,391
18 <151> PRIOR FILING DATE: 1999-05-21
20 <150> PRIOR APPLICATION NUMBER: US 09/352,159
21 <151> PRIOR FILING DATE: 1999-07-12
23 <150> PRIOR APPLICATION NUMBER: US 09/352,168
24 <151> PRIOR FILING DATE: 1999-07-12
26 <160> NUMBER OF SEQ ID NOS: 53
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32 <212> TYPE: DNA
33 <213> ORGANISM: Exophiala spinifera
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37 <222> LOCATION: (346)...(346)
38 <223> OTHER INFORMATION: n = A,T,C or G
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43 attgtcgatc gacgtcgatg ctgggtatctc tggcaaatga gatggggtca cagctcgatt 180
44 ggaggacgcc cgagaagcct tggtcgcgcc accacggcct gtcccatacg aagactatct 240
45 tgctatagta gcccgagata gaattttccg ccaatgcttg cttctcggcg ggaagagggtg 300
OK 46 gtgaaaatgt caaggtggga tacaagggtg tcggtaacga aaccancacc tttttgcttc 360
47 ggaacacggc gc 372
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56 tacaagggtg tcggtaacga aaccaccacc tttttgcttc ggaacacggc gcccgaggcc 120
57 gatcgactg tacagccgga tgccgactgc tcaatttcag cgaacgggggt gttgagggtgc 180
58 ac 182
60 <210> SEQ ID NO: 3
61 <211> LENGTH: 29
62 <212> TYPE: DNA
63 <213> ORGANISM: Artificial Sequence

RAW SEQUENCE LISTING

DATE: 02/08/2001

PATENT APPLICATION: US/09/771,045

TIME: 12:14:08

Input Set : A:\1134CSEQLIST.TXT

Output Set: N:\CRF3\02082001\I771045.raw

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66 <223> OTHER INFORMATION: Designed oligonucleotide for 3' RACE, N21965
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73 <211> LENGTH: 28
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75 <213> ORGANISM: Artificial Sequence
77 <220> FEATURE:
78 <223> OTHER INFORMATION: Designed oligonucleotide for 5' RACE, 21968
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90 <222> LOCATION: (1)...(1386)
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94   Asp Asn Val Ala Asp Val Val Val Val Gly Ala Gly Leu Ser Gly Leu
95   1      5      10      15
97   gag acg gca cgc aaa gtc cag gcc gcc ggt ctg tcc tgc ctc gtt ctt                96
98   Glu Thr Ala Arg Lys Val Gln Ala Ala Gly Leu Ser Cys Leu Val Leu
99   20      25      30
101  gag gcg atg gat cgt gta ggg gga aag act ctg agc gta caa tgg ggt                144
102  Glu Ala Met Asp Arg Val Gly Gly Lys Thr Leu Ser Val Gln Ser Gly
103  35      40      45
105  ccc ggc agg acg act atc aac gac ctc ggc gct gcg tgg atc aat gac                192
106  Pro Gly Arg Thr Thr Ile Asn Asp Leu Gly Ala Ala Trp Ile Asn Asp
107  50      55      60
109  agc aac caa agc gaa gta tcc aga ttg ttt gaa aga ttt cat ttg gag                240
110  Ser Asn Gln Ser Glu Val Ser Arg Leu Phe Glu Arg Phe His Leu Glu
111  65      70      75      80
113  ggc gag ctc cag agg acg act gga aat tca atc cat caa gca caa gac                288
114  Gly Glu Leu Gln Arg Thr Thr Gly Asn Ser Ile His Gln Ala Gln Asp
115  85      90      95
117  ggt aca acc act aca gct cct tat ggt gac tcc ttg ctg agc gag gag                336
118  Gly Thr Thr Thr Thr Ala Pro Tyr Gly Asp Ser Leu Leu Ser Glu Glu
119  100     105     110
121  gtt gca agt gca ctt gcg gaa ctc ctc ccc gta tgg tct cag ctg atc                384
122  Val Ala Ser Ala Leu Ala Glu Leu Leu Pro Val Trp Ser Gln Leu Ile
123  115     120     125
125  gaa gag cat agc ctt caa gac ctc aag gcg agc cct cag gcg aag cgg                432
126  Glu Glu His Ser Leu Gln Asp Leu Lys Ala Ser Pro Gln Ala Lys Arg
127  130     135     140
129  ctc gac agt gtg agc ttc gcg cac tac tgt gag aag gaa cta aac ttg                480
130  Leu Asp Ser Val Ser Phe Ala His Tyr Cys Glu Lys Glu Leu Asn Leu

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RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/771,045

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133	cct gct gtt ctc ggc gta gca aac cag atc aca cgc gct ctg ctc ggt	528			
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135	165 170 175				
137	gtg gaa gcc cac gag atc agc atg ctt ttt ctc acc gac tac atc aag	576			
138	Val Glu Ala His Glu Ile Ser Met Leu Phe Leu Thr Asp Tyr Ile Lys				
139	180 185 190				
141	agt gcc acc ggt ctc agt aat att ttc tcg gac aag aaa gac ggc ggg	624			
142	Ser Ala Thr Gly Leu Ser Asn Ile Phe Ser Asp Lys Lys Asp Gly Gly				
143	195 200 205				
145	cag tat atg cga tgc aaa aca ggt atg cag tcg att tgc cat gcc atg	672			
146	Gln Tyr Met Arg Cys Lys Thr Gly Met Gln Ser Ile Cys His Ala Met				
147	210 215 220				
149	tca aag gaa ctt gtt cca ggc tca gtg cac ctc aac acc ccc gtc gct	720			
150	Ser Lys Glu Leu Val Pro Gly Ser Val His Leu Asn Thr Pro Val Ala				
151	225 230 235 240				
153	gaa att gag cag tcg gca tcc ggc tgt aca gta cga tcg gcc tcg ggc	768			
154	Glu Ile Glu Gln Ser Ala Ser Gly Cys Thr Val Arg Ser Ala Ser Gly				
155	245 250 255				
157	gcc gtg ttc cga agc aaa aag gtg gtg gtt tcg tta ccg aca acc ttg	816			
158	Ala Val Phe Arg Ser Lys Lys Val Val Val Ser Leu Pro Thr Thr Leu				
159	260 265 270				
161	tat ccc acc ttg aca ttt tca cca cct ctt ccc gcc gag aag caa gca	864			
162	Tyr Pro Thr Leu Thr Phe Ser Pro Pro Leu Pro Ala Glu Lys Gln Ala				
163	275 280 285				
165	ttg gcg gaa aat tct atc ctg ggc tac tat agc aag ata gtc ttc gta	912			
166	Leu Ala Glu Asn Ser Ile Leu Gly Tyr Tyr Ser Lys Ile Val Phe Val				
167	290 295 300				
169	tgg gac aag ccg tgg tgg cgc gaa caa ggc ttc tcg ggc gtc ctc caa	960			
170	Trp Asp Lys Pro Trp Arg Glu Gln Gly Phe Ser Gly Val Leu Gln				
171	305 310 315 320				
173	tcg agc tgt gac ccc atc tca ttt gcc aga gat acc agc atc gac gtc	1008			
174	Ser Ser Cys Asp Pro Ile Ser Phe Ala Arg Asp Thr Ser Ile Asp Val				
175	325 330 335				
177	gat cga caa tgg tcc att acc tgt ttc atg gtc gga gac ccg gga cgg	1056			
178	Asp Arg Gln Trp Ser Ile Thr Cys Phe Met Val Gly Asp Pro Gly Arg				
179	340 345 350				
181	aag tgg tcc caa cag tcc aag cag gta cga caa aag tct gtc tgg gac	1104			
182	Lys Trp Ser Gln Gln Ser Lys Gln Val Arg Gln Lys Ser Val Trp Asp				
183	355 360 365				
185	caa ctc cgc gca gcc tac gag aac gcc ggg gcc caa gtc cca gag ccg	1152			
186	Gln Leu Arg Ala Ala Tyr Trp Glu Asn Ala Gly Ala Gln Val Pro Glu Pro				
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189	gcc aac gtg ctc gaa atc gag tgg tcg aag cag cag tat ttc caa gga	1200			
190	Ala Asn Val Leu Glu Ile Glu Trp Ser Lys Gln Gln Tyr Phe Gln Gly				
191	385 390 395 400				
193	gct ccg agc gcc gtc tat ggg ctg aac gat ctc atc aca ctg ggt tcg	1248			
194	Ala Pro Ser Ala Val Tyr Gly Leu Asn Asp Leu Ile Thr Leu Gly Ser				
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RAW SEQUENCE LISTING

DATE: 02/08/2001

PATENT APPLICATION: US/09/771,045

TIME: 12:14:08

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Output Set: N:\CRF3\02082001\I771045.raw

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199              420              425              430
201  tot tta gtt tgg aaa ggg tat atg gaa ggg gcc ata cga tcg ggt caa      1344
202  Ser Leu Val Trp Lys Gly Tyr Met Glu Gly Ala Ile Arg Ser Gly Gln
203              435              440              445
205  cga ggt gct gca gaa gtt gtg gct agc ctg gtg cca gca gca      1386
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214 <213> ORGANISM: Exophiala spinifera
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221  Glu Ala Met Asp Arg Val Gly Gly Lys Thr Leu Ser Val Gln Ser Gly
222      35      40      45
223  Pro Gly Arg Thr Thr Ile Asn Asp Leu Gly Ala Ala Trp Ile Asn Asp
224      50      55      60
225  Ser Asn Gln Ser Glu Val Ser Arg Leu Phe Glu Arg Phe His Leu Glu
226      65      70      75      80
227  Gly Glu Leu Gln Arg Thr Thr Gly Asn Ser Ile His Gln Ala Gln Asp
228      85      90      95
229  Gly Thr Thr Thr Thr Ala Pro Tyr Gly Asp Ser Leu Leu Ser Glu Glu
230      100      105      110
231  Val Ala Ser Ala Leu Ala Glu Leu Leu Pro Val Trp Ser Gln Leu Ile
232      115      120      125
233  Glu Glu His Ser Leu Gln Asp Leu Lys Ala Ser Pro Gln Ala Lys Arg
234      130      135      140
235  Leu Asp Ser Val Ser Phe Ala His Tyr Cys Glu Lys Glu Leu Asn Leu
236      145      150      155      160
237  Pro Ala Val Leu Gly Val Ala Asn Gln Ile Thr Arg Ala Leu Leu Gly
238      165      170      175
239  Val Glu Ala His Glu Ile Ser Met Leu Phe Leu Thr Asp Tyr Ile Lys
240      180      185      190
241  Ser Ala Thr Gly Leu Ser Asn Ile Phe Ser Asp Lys Lys Asp Gly Gly
242      195      200      205
243  Gln Tyr Met Arg Cys Lys Thr Gly Met Gln Ser Ile Cys His Ala Met
244      210      215      220
245  Ser Lys Glu Leu Val Pro Gly Ser Val His Leu Asn Thr Pro Val Ala
246      225      230      235      240
247  Glu Ile Glu Gln Ser Ala Ser Gly Cys Thr Val Arg Ser Ala Ser Gly
248      245      250      255
249  Ala Val Phe Arg Ser Lys Lys Val Val Ser Leu Pro Thr Thr Leu
250      260      265      270

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RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/771,045

DATE: 02/08/2001

TIME: 12:14:08

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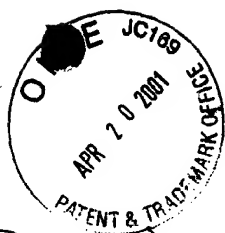
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253 Leu Ala Glu Asn Ser Ile Leu Gly Tyr Tyr Ser Lys Ile Val Phe Val
254      290      295      300
255 Trp Asp Lys Pro Trp Trp Arg Glu Gln Gly Phe Ser Gly Val Leu Gln
256      305      310      315      320
257 Ser Ser Cys Asp Pro Ile Ser Phe Ala Arg Asp Thr Ser Ile Asp Val
258      325      330      335
259 Asp Arg Gln Trp Ser Ile Thr Cys Phe Met Val Gly Asp Pro Gly Arg
260      340      345      350
261 Lys Trp Ser Gln Gln Ser Lys Gln Val Arg Gln Lys Ser Val Trp Asp
262      355      360      365
263 Gln Leu Arg Ala Ala Tyr Glu Asn Ala Gly Ala Gln Val Pro Glu Pro
264      370      375      380
265 Ala Asn Val Leu Glu Ile Glu Trp Ser Lys Gln Gln Tyr Phe Gln Gly
266      385      390      395      400
267 Ala Pro Ser Ala Val Tyr Gly Leu Asn Asp Leu Ile Thr Leu Gly Ser
268      405      410      415
269 Ala Leu Arg Thr Pro Phe Lys Ser Val His Phe Val Gly Thr Glu Thr
270      420      425      430
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286 <222> LOCATION: (647)...(699)
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294 1      5      10      15
296 gag acg gca cgc aaa gtc cag gcc gcc ggt ctg tcc tgc ctc gtt ctt      96
297 Glu Thr Ala Arg Lys Val Gln Ala Ala Gly Leu Ser Cys Leu Val Leu
298      20      25      30
300 gag gcg atg gat cgt gta ggg gga aag act ctg agc gta caa tcg ggt      144
301 Glu Ala Met Asp Arg Val Gly Gly Lys Thr Leu Ser Val Gln Ser Gly
302      35      40      45
304 ccc ggc agg acg act atc aac gac ctc ggc gct gcg tgg atc aat gac      192
305 Pro Gly Arg Thr Thr Ile Asn Asp Leu Gly Ala Ala Trp Ile Asn Asp
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308 agc aac caa agc gaa gta tcc aga ttg ttt gaa aga ttt cat ttg gag      240

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<212> PRT
<213> Unknown
<400> 19



09/771,045 6

see item 12 on Encl Summary Sheet



The types of errors shown exist throughout the Sequence Listing. Please check subsequent sequences for similar errors.

FI

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

VERIFICATION SUMMARY

PATENT APPLICATION: US/09/771,045

DATE: 02/08/2001

TIME: 12:14:09

Input Set : A:\1134CSEQLIST.TXT

Output Set: N:\CRF3\02082001\I771045.raw

L:14 M:270 C: Current Application Number differs, Replaced Current Application No
 L:14 M:271 C: Current Filing Date differs, Replaced Current Filing Date
 L:46 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
 L:349 M:361 W: Invalid Split Codon, Sequence data for SEQ ID#: 7
 L:1234 M:258 W: Mandatory Feature missing, <220> FEATURE:
 L:1234 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
 L:1334 M:259 W: Allowed number of lines exceeded, <223> Other Information:
 L:1335 M:259 W: Allowed number of lines exceeded, <223> Other Information:
 L:1488 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
 L:2095 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
 L:2517 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
 L:2989 M:258 W: Mandatory Feature missing, <220> FEATURE:
 L:2989 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
 L:3153 M:259 W: Allowed number of lines exceeded, <223> Other Information:
 L:3154 M:259 W: Allowed number of lines exceeded, <223> Other Information:
 L:3487 M:258 W: Mandatory Feature missing, <220> FEATURE:
 L:3487 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
 L:3810 M:258 W: Mandatory Feature missing, <220> FEATURE:
 L:3810 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
 L:4185 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:39
 L:4247 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:40



Raw Sequence Listing Error Summary

ERROR DETECTED SUGGESTED CORRECTION

SERIAL NUMBER:

09/77/045

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 Wrapped Nucleics The number/text at the end of each line "wrapped" down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".
- 2 Wrapped Aminos The amino acid number/text at the end of each line "wrapped" down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".
- 3 Incorrect Line Length The rules require that a line not exceed 72 characters in length. This includes spaces.
- 4 Misaligned Amino Acid Numbering The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs between the numbering. It is recommended to delete any tabs and use spacing between the numbers.
- 5 Non-ASCII This file was not saved in ASCII (DOS) text, as required by the Sequence Rules.
Please ensure your subsequent submission is saved in ASCII text so that it can be processed.
- 6 Variable Length Sequence(s) contain n's or Xaa's which represented more than one residue.
As per the rules, each n or Xaa can only represent a single residue.
Please present the maximum number of each residue having variable length and indicate in the (ix) feature section that some may be missing.
- 7 PatentIn ver. 2.0 "bug" A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequence(s) . Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies primarily to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
- 8 Skipped Sequences (OLD RULES) Sequence(s) missing. If intentional, please use the following format for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X:
(i) SEQUENCE CHARACTERISTICS:(Do not insert any headings under "SEQUENCE CHARACTERISTICS")
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X:
This sequence is intentionally skipped

Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s).
- 9 Skipped Sequences (NEW RULES) Sequence(s) missing. If intentional, please use the following format for each skipped sequence.
<210> sequence id number
<400> sequence id number
000
- 10 Use of n's or Xaa's (NEW RULES) Use of n's and/or Xaa's have been detected in the Sequence Listing.
Use of <220> to <223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 11 Use of <213>Organism (NEW RULES) Sequence(s) are missing this mandatory field or its response.
- 12 J Use of <220>Feature (NEW RULES) Sequence(s) 19 and more are missing the <220>Feature and associated headings.
Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial" or "Unknown"
Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of new Rules)
- 13 PatentIn ver. 2.0 "bug" Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing).
Instead, please use "File Manager" or any other means to copy file to floppy disk.